

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/037,657B
Source: 1fw16
Date Processed by STIC: 2/20/06

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IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/037,657B

DATE: 07/20/2006
TIME: 16:44:14

Input Set : A:\10857Z.SEQ.txt
Output Set: N:\CRF4\07202006\I037657B.raw

4 <110> APPLICANT: Hilton, Douglas J.
 5 Nicola, Nicos A.
 6 Farley, Alison
 7 Wilson, Tracy
 8 Zhang, Jian-Guo
 9 Alexander, Warren
 10 Rakar, Steven
 11 Fabri, Louis
 12 Kojima, Tetsuo
 13 Maeda, Masatsugu
 14 Kikuchi, Yasufumi
 15 Nash, Andrew
 17 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
 18 ENCODING SAME
 20 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
 22 <140> CURRENT APPLICATION NUMBER: 09/037,657B
 23 <141> CURRENT FILING DATE: 1998-03-10
 25 <150> PRIOR APPLICATION NUMBER: 08/928,720
 26 <151> PRIOR FILING DATE: 1997-09-11
 28 <160> NUMBER OF SEQ ID NOS: 58
 30 <170> SOFTWARE: PatentIn Ver. 2.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 5
 34 <212> TYPE: PRT
 35 <213> ORGANISM: Unknown
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Description of Unknown Organism: haemopoietin receptor
 40 <220> FEATURE:
 41 <221> NAME/KEY: UNSURE
 42 <222> LOCATION: (3)
 43 <223> OTHER INFORMATION: Unsure at position 3
 45 <400> SEQUENCE: 1
 W--> 46 Trp Ser Xaa Trp Ser
 47 5
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 24
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Artificial Sequence
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
 59 <400> SEQUENCE: 2
 60 actcgctcca gattccggcc tttt
 63 <210> SEQ ID NO: 3

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64 <211> LENGTH: 24
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Description of Artificial Sequence:M108 probe
71 <400> SEQUENCE: 3
72 tcccgccctt ttcgaccat agat 24
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 24
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
83 <400> SEQUENCE: 4
84 ggtacttggc ttggaagagg aaat 24
87 <210> SEQ ID NO: 5
88 <211> LENGTH: 24
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
95 <400> SEQUENCE: 5
96 cggctcacgt gcacgtcggg tggg 24
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 22
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
107 <400> SEQUENCE: 6
108 agctgctgtt aaagggtttc tc 22
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 15
113 <212> TYPE: DNA
114 <213> ORGANISM: Unknown
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
120 <220> FEATURE:
121 <221> NAME/KEY: unsure
122 <222> LOCATION: (1)
123 <223> OTHER INFORMATION: Unsure at position 1
125 <220> FEATURE:
126 <221> NAME/KEY: unsure
127 <222> LOCATION: (7)
128 <223> OTHER INFORMATION: Unsure at position 7
130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (10)
133 <223> OTHER INFORMATION: Unsure at position 10

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135 <400> SEQUENCE: 7
136 rctccartcr ctcca 15
139 <210> SEQ ID NO: 8
140 <211> LENGTH: 15
141 <212> TYPE: DNA
142 <213> ORGANISM: Unknown
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Description of Unknown Organism:Unsure
147 <220> FEATURE:
148 <221> NAME/KEY: unsure
149 <222> LOCATION: (1)
150 <223> OTHER INFORMATION: Unsure at position 1
152 <220> FEATURE:
153 <221> NAME/KEY: unsure
154 <222> LOCATION: (7)
155 <223> OTHER INFORMATION: Unsure at position 7
157 <220> FEATURE:
158 <221> NAME/KEY: unsure
159 <222> LOCATION: (10)
160 <223> OTHER INFORMATION: Unsure at position 10
162 <400> SEQUENCE: 8 15
163 rctccaytcr ctcca
166 <210> SEQ ID NO: 9
167 <211> LENGTH: 21
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
174 <400> SEQUENCE: 9
175 aagtgtgacc atcatgtgga c 21
178 <210> SEQ ID NO: 10
179 <211> LENGTH: 18
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
186 <400> SEQUENCE: 10
187 ggaggtgtta aggaggcg 18
190 <210> SEQ ID NO: 11
191 <211> LENGTH: 18
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
198 <400> SEQUENCE: 11
199 atccccgcgg gtcgcccc 18
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 1629
204 <212> TYPE: DNA

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205 <213> ORGANISM: Unknown
 207 <220> FEATURE:
 208 <221> NAME/KEY: CDS
 209 <222> LOCATION: (124)..(1362)
 211 <220> FEATURE:
 212 <223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1
 214 <400> SEQUENCE: 12
 215 ggcacgagct tcgctgtccg cgcccagtga cgcgctgctgac gacccgagcc ccaatctgca 60
 217 cccccgagac tcgccccccgc cccataccgg cgttcagtc accgcccgtt gcgccacc 120
 219 ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 168
 220 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
 221 1 5 10 15
 223 ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc 216
 224 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
 225 20 25 30
 227 ctc ggg gtg cct ccg ggc gga tcg gga gcc cac aca gct gta atc agc 264
 228 Leu Gly Val Pro Arg Gly Ser Gly Ala His Thr Ala Val Ile Ser
 229 35 40 45
 231 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
 232 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
 233 50 55 60
 235 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
 236 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
 237 65 70 75
 239 acc ctc aat ggt ccg ccg ctg ccc tct gag ctg tcc ccg ctc ctt aac 408
 240 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 241 80 85 90 95
 243 acc tcc acc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
 244 Thr Ser Thr Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
 245 100 105 110
 247 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
 248 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
 249 115 120 125
 251 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
 252 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
 253 130 135 140
 255 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc ccg tgg aca 600
 256 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 257 145 150 155
 259 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
 260 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
 261 160 165 170 175
 263 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
 264 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
 265 180 185 190
 267 act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
 268 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
 269 195 200 205
 271 act ccc tat gag atc tgg gtg gaa gcc acc aat ccg cta ggc tca gca 792

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272	Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala			
273	210	215	220	
275	aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac	840		
276	Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp			
277	225	230	235	
279	ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag	888		
280	Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln			
281	240	245	250	255
283	ctg agt gtg cgc tgg gtc tca cca gct ctc aag gat ttc ctc ttc	936		
284	Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe			
285	260	265	270	
287	caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg	984		
288	Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp			
289	275	280	285	
291	aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc	1032		
293	Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly			
294	290	295	300	
296	ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc	1080		
297	Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe			
298	305	310	315	
300	ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac	1128		
301	Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His			
302	320	325	330	335
304	ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc	1176		
305	Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly			
306	340	345	350	
308	ggg gtg tgc gag ccg cgg ggc gag ccc agc tcg ggc ccg gtg cgg	1224		
309	Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg			
310	355	360	365	
312	cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc	1272		
313	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys			
314	370	375	380	
316	tgc aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag	1320		
317	Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln			
318	385	390	395	
320	aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc	1362		
321	Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu			
322	400	405	410	
324	taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagccct	1422		
326	ctgtaccatc tggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa	1482		
328	ccacagctt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaagggttgg	1542		
330	ggtattgcag ggcctcccaa caatctctt aaataaataa aggagttgtt caggtaaaaa	1602		
332	aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaa	1629		
335	<210> SEQ ID NO: 13			
336	<211> LENGTH: 413			
337	<212> TYPE: PRT			
338	<213> ORGANISM: Unknown			
340	<220> FEATURE:			
341	<223> OTHER INFORMATION: Description of Unknown Organism:Murine NR6.1			

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/20/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3
Seq#:29; Xaa Pos. 136,139,162,177

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:21; Line(s) 949

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:45